

WEST Search History

[Hide Items](#)
[Restore](#)
[Clear](#)
[Cancel](#)

DATE: Tuesday, July 25, 2006

Hide?	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=NO; OP=ADJ</i>	
<input type="checkbox"/>	L6	(((ailim or icos or 8f4 or jtt\$ or crp1 or crp-1) not icos.as.) with inflammat\$.clm.	1
<input type="checkbox"/>	L5	(((ailim or icos or 8f4 or jtt\$ or crp1 or crp-1) not icos.as.) with inflammat\$	54
<input type="checkbox"/>	L4	(((ailim or icos or 8f4 or jtt\$ or crp1 or crp-1) not icos.as.) same inflammat\$	127
<input type="checkbox"/>	L3	(((ailim or icos or 8f4 or jtt\$ or crp1 or crp-1) not icos.as.) and inflammat\$	1029
<input type="checkbox"/>	L2	(((ailim or icos or 8f4 or jtt\$ or crp1 or crp-1).not icos.as.) and (tamatanit\$ or tezuka-k\$).in.)	27
		<i>DB=PGPB,USPT; THES=ASSIGNEE; PLUR=NO; OP=ADJ</i>	
<input type="checkbox"/>	L1	(((ailim or icos or 8f4 or jtt\$ or crp1 or crp-1) not icos.as.) and (tamatanit\$ or tezuka-k\$).in.)	19

END OF SEARCH HISTORY

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.rag.

[Score Home](#)
[Page](#)

Retrieve Application List

SCORE System Overview

SCORE
FAQ

Comments /
Suggestions

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.rag.

start

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

```
Run on:      May 26, 2006, 11:11:28 ; Search time 431.325 Seconds
              (without alignments)
              210.945 Million cell updates/sec
```

```
Title:          US-10-723-602-2
Perfect score:  1082
Sequence:       1 MKSGLWYFFLFCLRIKVLTG.....YMFMRVNTAKKSRLTDVTL 199
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.ra1.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.ra1.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2006, 11:27:41 ; Search time 90.4545 Seconds
(without alignments)
192.567 Million cell updates/sec

Title: US-10-723-602-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLFCLRIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.ra

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.ra.pbm.

[start](#)

[Go Back to pr](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2006, 11:28:37 ; Search time 296.12 Seconds
(without alignments)
311.292 Million cell updates/sec

Title: US-10-723-602-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLFCLRIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1082	100.0	199	3	US-09-833-245-113	Sequence 113, App
2	1082	100.0	199	3	US-09-833-245-114	Sequence 114, App
3	1082	100.0	199	4	US-10-107-828-2	Sequence 2, Appli

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.rapbn

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.rapbn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2006, 11:30:16 ; Search time 17.1388 Seconds
(without alignments)
129.317 Million cell updates/sec

Title: US-10-723-602-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLFCLRIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1082	100.0	199	6	US-10-511-937-2440	Sequence 2440, Ap

SCORE Search R

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-7:
[start](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2006, 11:19:42 ; Search time 55.2249 Seconds
(without alignments)
346.712 Million cell updates/sec

Title: US-10-723-602-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLFCLRIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1082	100.0	199	2 S78540	inducible T-cell c
2	701	64.8	200	2 JC7397	activation-inducib
3	696	64.3	216	2 JC7396	activation-inducib
4	152	14.0	218	2 S24413	T-cell surface gly
5	150.5	13.9	221	2 I46689	CD28 precursor - r
6	139.5	12.9	173	2 I46197	cell surface prote
7	139.5	12.9	220	1 RWHU28	T-cell surface gly
8	138	12.8	218	2 A43523	T-cell surface gly

SCORE Search Results Details for Application 10723602 and Search Result us-10-723-602-2.rup.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10723602 and Search Result us-10-723-602-2.rup.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 26, 2006, 11:11:46 ; Search time 453.225 Seconds
(without alignments)
406.152 Million cell updates/sec

Title: US-10-723-602-2
Perfect score: 1082
Sequence: 1 MKSGLWYFFLFCLRIKVLTG.....YMFMRVNTAKKSRLTDVTL 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1082	100.0	199	1	ICOS_HUMAN	Q9y6w8 homo sapien
2	1082	100.0	199	2	Q53QY6_HUMAN	Q53qy6 homo sapien
3	804.5	74.4	209	2	Q2KMN0_PIG	Q2kmn0 sus scrofa
4	788.5	72.9	209	1	ICOS_BOVIN	Q58df9 bos taurus